SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lincoln, Steve
Klinger, Tod M.
Au-Young, Janice
Tang, Y. Tom
Goold, Richard
Akerblom, Ingrid E.
Seilhamer, Jeffrey J.
Hawkins, Phillip R.
Murry, Lynn E.
Delegeane, Angelo M.
Levine, Wendy B.
Hillman, Jennifer L.
Goli, Surya K.
Altus, Christina M.
Bandman, Olga
LaBrie, Samuel T.
Shah, Purvi

(ii) TITLE OF THE INVENTION: Database for Storage and Analysis of Full
Length Sequences

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Bozicevic & Reed, L.L.P.
(B) STREET: 285 Hamilton Ave.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: U.S.
(F) ZIP: 94301

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/282,955
(B) FILING DATE: July 29, 1995

(A) APPLICATION NUMBER: 08/187,530
(B) FILING DATE: January 27, 1994

(A) APPLICATION NUMBER: 08/179,873
(B) FILING DATE: January 11, 1994

(A) APPLICATION NUMBER: 08/100,523

(B) FILING DATE: August 3, 1993

(A) APPLICATION NUMBER: 07/977,780
(B) FILING DATE: November 19, 1992

(A) APPLICATION NUMBER: 07/916,491
(B) FILING DATE: July 17, 1992

(A) APPLICATION NUMBER: 08/289,822
(B) FILING DATE: August 12, 1994

(A) APPLICATION NUMBER: 08/581,240
(B) FILING DATE: December 29, 1995

(A) APPLICATION NUMBER: 08/657,697
(B) FILING DATE: May 29, 1996

(A) APPLICATION NUMBER: 08/747,547
(B) FILING DATE: November 12, 1996

(A) APPLICATION NUMBER: 08/712,710
(B) FILING DATE: September 12, 1996

(A) APPLICATION NUMBER: 08/744,026
(B) FILING DATE: November 5, 1996

(A) APPLICATION NUMBER: 08/786,999
(B) FILING DATE: January 23, 1997

(A) APPLICATION NUMBER: 08/822,262
(B) FILING DATE: March 20, 1997

(A) APPLICATION NUMBER: 08/000,000 (as yet unassigned)
(B) FILING DATE: October 16, 1997

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Francis, Carol L.
  (B) REGISTRATION NUMBER: 36,513
  (C) REFERENCE/DOCKET NUMBER: 6514/069001

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 650-327-3400
  (B) TELEFAX: 650-327-3231

    (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 373 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
    (A) LIBRARY: Pancreatic Cancer

            (B) CLONE: PANC1A

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 GTACGGAGGT GAGGTTTGTN ACCGCGATTC TAAGAGGTGG GCTTTTAGTC CCTCCAGACC   60
   TCGGCTTTAG TGCTGTCTCC GCTTTTYTTT CACCTTCACA GAGGTTCGTG TCTTCCTAAA   120
   AGAAGGTTTT ATTGGGAGGT AAAGGTCAAT GCGTAGGGGT AGAGTAAGAT GTCTTATGGT   180
   GAAATTRAAG GTAAATTCTT GGGACCTAGA GAAGAAGTAA CGAGTGAGCC ACGCTGTAAA   240
   AAATTGAAGT CAACCACAGA GTCGTATGTT TTTCACAATC ATAGTAATGC TGATTTTCAC   300
10 AGNATCCAAG AGAAAACTGG AAATGATTGG GTCCCTGTGN NCATCATTGA TGTCAGAGGA   360
   CATAGTTATT TGC   373

            (2) INFORMATION FOR SEQ ID NO:2:
15
        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 321 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
20   (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA

       (vii) IMMEDIATE SOURCE:
25   (A) LIBRARY: Pancreatic Cancer
           (B) CLONE: PANC1B

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 GTGAGGTTTG TTACCNCGAT TCTGAGAGGT GGGCTTTTAG TCCCTCCAGA CCTCGGCTTT   60
   AGTGCTGTCT CCGMTTTTCT TTCACCTTCA CAGAGATGTC TTATGGTGAA ATTGAAGGTA   120
   AATTCTTGGG ACCTAGWGAA GAAGTAACGA GTGAGCCACG CTGTAAAAAA TTGAAGTCAA   180
   CCACAGAGTC GTATGTTTTT CACAATCATA GTAATGCTGA TTTTCACAGW ATCCAAGAGA   240
   AAACTGGAAA TGATTTGGGT CCCTGTGACC ATCATTNATG TCAGAGGNCA TAGTTAATTT   300
35 GCAGGAGANC AAAAATCAAA A   321

            (2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 528 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

45   (ii) MOLECULE TYPE: cDNA

       (vii) IMMEDIATE SOURCE:
           (A) LIBRARY: NEUTGMT01
           (B) CLONE: 637393
50
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

   ATGACAGACT GTGAATTTGG ATATATTTAC AGGCTGGCTC AGGACTATCT GCAGTGCGTC   60
   CTACAGATAC CACAACCTGG ATCAGGTCCA AGCAAAACGT CCAGAGTGCT ACAAAATGTT   120
55 GCGTTCTCAG TCCAAAAAGA AGTGGAAAAG AATCTGAAGT CATGCTTGGA CAATGTTAAT   180
   GTTGTGTCCG TAGACACTGC CAGAACACTA TTCAACCAAG TGATGGAAAA GGAGTTTGAA   240
   GACGACATCA TTAACTGGGG AAGAATTGTA ACCATATTTG CATTTGAAGG TATTCTCATC   300

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     AAGAAACTTC TACGACAGCA AATTGCCCCG GATGTGGATA CCTATAAGGA GATTTCATAT      360
     TTTGTTGCGG AGTTCATAAT GAATAACACA GGAGAATGGA TAAGGCAAAA CGGAGGCTGG      420
     GAAAATGGCT TTGTAAAGAA GTTTGAACCT AAATCTGGCT GGATGACTTT TCTAGAAGTT      480
     ACAGGAAAGA TCTGTGAAAT GCTATCTCTC CTGAAGCAAT ACTGTTGA                   528
 5
```

     (2) INFORMATION FOR SEQ ID NO:4:

         (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 405 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

15   (ii) MOLECULE TYPE: cDNA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
20 GTCCAAATCA CTCATTGTTT GTGAAAGCTG AGCTCACAGC AAAACAAGCC ACCATGAAGC      60
   TGTCGGTGTG TCTCCTGCTG GTCACGCTGG CCCTCTGCTG CTACCAGGCC AATGCCGAGT      120
   TCTGCCCAGC TCTTGTTTCT GAGCTGTTAG ACTTCTTCTT CATTAGTGAA CCTCTGTTCA      180
   AGTTAAGTCT TGCCAAATTT GATGCCCCTC CGGAAGCTGT TGCAGCCAAG TTAGGAGTGA      240
   AGAGATGCAC GGATCAGATG TCCCTTCAGA AACGAAGCCT CATTGCGGAA GTCCTGGTGA      300
25 AAATATTGAA GAAATGTAGT GTGTGACATG TAAAAACTTT CATCCTGGTT TCCACTGTCT      360
   TTCAATGACA CCCTGATCTT CACTGCAGAA TGTAAAGGTT TCAAC                     405
```


30 (2) INFORMATION FOR SEQ ID NO:5:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 495 base pairs
             (B) TYPE: nucleic acid
35   (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: cDNA

40   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
   GATCCTTGCC ACCCGCGACT GAACACCGAC AGCAGCAGCC TCACCATGAA GTTGCTGATG      60
   GTCCTCATGC TGGCGGCCCT CTCCCAGCAC TGCTACGCAG GCTCTGGCTG CCCCTTATTG      120
   GAGAATGTGA TTTCCAAGAC AATCAATCCA CAAGTGTCTA AGACTGAATA CAAAGAACTT      180
45 CTTCAAGAGT TCATAGACGA CAATGCCACT ACAAATGCCA TAGATGAATT GAAGGAATGT      240
   TTTCTTAACC AAACGGATGA AACTCTGAGC AATGTTGAGG TGTTTATGCA ATTAATATAT      300
   GACAGCAGTC TTTGTGATTT ATTTTAACTT TCTGCAAGAC CTTTGGCTCA CAGAACTGCA      360
   GGGTATGGTG AGAAACCAAC TACGGATTGC TGCAAACCAC ACCTTCTCTT TCTTATGTCT      420
   TTTTACTACA AACTACAAGA CAATTGTTGA AACCTGCTAT ACATGTTTAT TTTAATAAAT      480
50 TGATGGCAAA AACTG                                                        495
```


     (2) INFORMATION FOR SEQ ID NO:6:

55   (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 1143 base pairs
         (B) TYPE: nucleic acid

```
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (vii) IMMEDIATE SOURCE:
     (A) LIBRARY:
     (B) CLONE: Consensus

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCCCCGCCG CGCCCGGCGC GCCCGCCGCC CGGGGGGATG TCTTACAAAC CGAACTTGGC    60
CGCGCACATG CCCGCCGCCG CCCTCAACGC CGCTGGGAGT GTCCACTCGC CTTCCACCAG   120
CATGGCAACG TCTTCACAGT ACCGCCAGCT GCTCAGTGAC TACGGGCCAC CGTCCCTAGG   180
CTACACCCAG GGAACTGGGA ACAGCCAGGT GCCCCAAAGC AAATACGCGG AGCTGCTGGC   240
CATCATTGAA GAGCTGGGGA AGGAGATCAG ACCCACGTAC GCAGGGAGCA AGAGTGCCAT   300
GGAGAGGCTG AAGCGCGGCA TCATTCACGC TAGAGGACTG GTTCGGGAGT TCTTGGCAGA   360
AACGGAACGG AATGCCAGAT CCTAGCTGCC TTGTTGGTTT TGAAGGATTT CCATCTTTTT   420
ACAAGATGAG AAGTTACAGT TCATCTCCCC TGTTCAGATG AAACCCTTGT TTTCAAAATG   480
GTTACAGTTT CGTTTTTCCT CCCATGGTTC ACTTGGCTCT GAACCTACAG TCTCAAAGAT   540
TGAGAAAAGA TTTTGCAGTT AATTAGGATT TGCATTTTAA GTAGTTAGGA ACTGCCCAGG   600
TTTTTTTTGT TTTTTAAGCA TTGATTTAAA AGATGCACGG AAAGTTATCT TACAGCAAAC   660
TGTAGTTTGC CTCCAAGACA CCATTGTCTC CCTTTAATCT TCTCTTTTGT ATACATTTGT   720
TACCCATGGT GTTCTTTGTT CCTTTTCATA AGCTAATACC ACTGTAGGGA TTTTGTTTTG   780
AACGCATATT GACAGCACGC TTTACTTAGT AGCCGGTTCC CATTTGCCAT ACAATGTAGG   840
TTCTGCTTAA TGTAACTTCT TTTTTGCTTA AGCATTTGCA TGACTATTAG TGCTTCAAAG   900
TCAATTTTTA AAAATGCACA AGTTATAAAT ACAGAAGAAA GAGCAACCCA CCAAACCTAA   960
CAAGGACCCC CGAACACTTT CATACTAAGA CTGTAAGTAG ATCTCAGTTC TGCGTTTATT  1020
GTAAGTTGAT AAAAACATCT GGAAGAAAAT GACTAAAACT GTTTGCATCT TTGTATGTAT  1080
TTATTACTTG ATGTAATAAA GCTTATTTTC ATTAACAATT TGTATTAAAA TGTGGGTTCC  1140
TTG                                                                1143


   (2) INFORMATION FOR SEQ ID NO:7:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 871 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (vii) IMMEDIATE SOURCE:
     (A) LIBRARY:
     (B) CLONE: Consensus

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACCTGCTGGC CCCTGGACAC CTCTGTCACC ATGTGGTTCC TGGTTCTGTG CCTCGCCCTG    60
TCCCTGGGGG GGACTGGTGC TGCGCCCCCG ATTCAGTCCC GGATTGTGGG AGGCTGGGAG   120
TGTGAGCAGC ATTCCCAGCC CTGGCAGGCG GCACTGGTCA TGGAAAACGA ATTGTTCTGC   180
TCGGGCGTCC TGGTGCATCC GCAGTGGGTG CTGTCAGCCG CACACTGTTT CCAGAACTCC   240
TACACCATCG GGCTGGGCCT GCACAGTCTT GAGGCCGACC AAGAGCCAGG GAGCCAGATG   300
GTGGAGGCCA GCCTCTCCGT ACGGCACCCA GAGTACAACA GACCCTTGCT CGCTAACGAC   360
CTCATGNTCA TCAAGTTGGA CGAATCCGTG TCCGAGTCTG ACAACATCCG GAGNATCAGC   420
ATTGNTTCGC AGTGCCCTAC CGCGGGGAAC TTTTGCCTCG TTTCTGGCTG GGGTCTGCTG   480
```

```
GCGAACGGCA GAATGCCTAC CGTGCTGCAG TGCGTGAACG TGTCGGTGGT GTCTGAGGAG    540
GTCTGCAGTA AGCTCTATGA CCCGCTGTAC CACCCCAGCA TGTTCTGCGC CGGCGGAGGG    600
CAAGACCAGA AGGACTCCTG CAACGGTGAC TCTGGGGGGC CCCTGATCTG CAACGGGTAC    660
TTGCAGGGCC TTGTGTCTTT CGGAAAAGCC CCGTGTGGCC AAGTTGGCGT GCCAGGTGTC    720
TACACCAACC TCTGCAAATT CACTGAGTGG ATAGAGAAAA CCGTCCAGGC CAGTTAACTC    780
TGGGGACTGG GAACCCATGA AATTGACCCC CAAATACATC CTGCGGAAGG AATTCAGGAA    840
TATCTGTTCC CAGCCCCTCC TCCCTCAGGC C                                   871
```

        (2) INFORMATION FOR SEQ ID NO:8:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1428 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (vii) IMMEDIATE SOURCE:
           (A) LIBRARY: Colnnot01
           (B) CLONE: 609476

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
GGCCGGGTTG GGGGTGTGCG ATTGTGTGGG ACGGTCTGGG GCAGCCCAGC AGCGGCTGAC     60
CCTCTGCCTG CGGGGAAGGG AGTCGCCAGG CGGCCGTCAT GGCGGTGTCG GAGAGCCAGC    120
TCAAGAAAAT GGTGTCCAAG TACAAATACA GAGACCTAAC TGTACGTGAA ACTGTCAATG    180
TTATTACTCT ATACAAAGAT CTCAAACCTG TTTTGGATTC ATATGTTTTT AACGATGGCA    240
GTTCCAGGGA ACTAATGAAC CTCACTGGAA CAATCCCTGT GCCTTATAGA GGTAATACAT    300
ACAATATTCC AATATGCCTA TGGCTACTGG ACACATACCC ATATAATCCC CCTATCTGTT    360
TTGTTAAGCC TACTAGTTCA ATGACTATTA AAACAGGAAA GCATGTTGAT GCAAATGGGA    420
AGATATATCT TCCTTATCTA CATGAATGGA AACACCCACA GTCAGACTTG TTGGGGCTTA    480
TTCAGGTCAT GATTGTGGTA TTTGGAGATG AACCTCCAGT CTTCTCTCGT CCTATTTCGG    540
CATCCTATCC GCCATACCAG GCAACGGGGC CACCAAATAC TTCCTACATG CCAGGCATGC    600
CAGGTGGAAT CTCTCCATAC CCATCCGGAT ACCCTCCCAA TCCCAGTGGT TACCCAGGCT    660
GTCCTTACCC ACCTGGTGGT CCATATCCTG CCACAACAG TTCTCAGTAC CCTTCTCAGC    720
CTCCTGTGAC CACTGTTGGT CCCAGTAGGG ATGGCACAAT CAGCGAGGAC ACCATCCGAG    780
CCTCTCTCAT CTCTGCGGTC AGTGACAAAC TGAGATGGCG GATGAAGGAG GAAATGGATC    840
GTGCCCAGGC AGAGCTCAAT GCCTTGAAAC GAACAGAAGA AGACCTGAAA AAGGGTCACC    900
AGAAACTGGA AGAGATGGTT ACCCGTTTAG ATCAAGAAGT AGCCGAGGTT GATAAAAACA    960
TAGAACTTTT GAAAAAGAAG GATGAAGAAC TCAGTTCTGC TCTGGAAAAA ATGGAAAATC   1020
AGTCTGAAAA CAATGATATC GATGAAGTTA TCATTCCCAC AGCTCCCTTA TACAAACAGA   1080
TCCTGAATCT GTATGCAGAA GAAAACGCTA TTGAAGACAC TATCTTTTAC TTGGGAGAAG   1140
CCTTGAGAAG GGGCGTGATA GACCTGGATG TCTTCCTGAA GCATGTACGT CTTCTGTCCC   1200
GTAAACAGTT CCAGCTGAGG GCACTAATGC AAAAAGCAAG AAAGACTGCC GGTCTCAGTG   1260
ACCTCTACTG ACTTCTCTGA TACCAGCTGG AGGTTGAGCT CTTCTTAAAG TATTCTTCTC   1320
TTCCTTTTAT CAGTAGGTGC CCAGAATAAG TTATTGCAGT TTATCATTCA MGTGTAAAAT   1380
ATTTTGAATC AATAATATAT TTTCTGTTTT CTTTTGGTAA AGATGGAT              1428
```

        (2) INFORMATION FOR SEQ ID NO:9:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 667 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (vii) IMMEDIATE SOURCE:

(A) LIBRARY: THPINOT03
(B) CLONE: 2446131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

5

```
GGCTGAGCGG CCCCGCAGCC AACCCCCGAG GAGCGGCCGG CTGGCGTCCG CCGCGCCCAG    60
GAGTTGGGGA TGTCCTACAA ACCCATCGCC CCTGCTCCCA GCAKCACCCC TGGCTCCAGC   120
ACCCCTGGGC CGGGCACCCC GGTCCCTACA GGAAGCGTCC CGTCGCCGTC GGGCTCAGTG   180
CCAGGAGCCG GCGCTCCTTT CAGACCGCTG TTTAACGACT TTGGACCGCC TTCCATGGGC   240
TACGTGCAGG CGATGAAGCC ACCCGGCGCC CAGGGCTCCC AGAGCACCTA CACGGACCTG   300
CTGTCAGTCA TAGAGGAGAT GGGCAAAGAG ATCCGGCCTA CCTATGCTGG CAGCAAGAGC   360
GCCATGGAGC GCCTGAAGAG AGGTATCATC CATGCCCGGG CCCTAGTCAG AGAGTGCCTG   420
GCAGAGACAG AGCGGAACGC CCGCACGTAA CAGGAAGCGC CTCGGCCTCA GCGTCTGGAC   480
CTATCCGGCC ACTGCAGAGC ACCCGCTTCT CCCTGGCCTT CATCCCGAGT TGCACTAACC   540
ATCCTGGGCT TCCTGTCCTG TGTCCCTTGG TGGGTCCCCT CCAGGAACCA AGGAGTGGCC   600
CTCCAGGTGG CAGCACTAAG GACACCCCCC CACAACAAGA GTTAGCAGCG AGGTCCCCAT   660
GAGTCCC                                                             667
```

(2) INFORMATION FOR SEQ ID NO:10: -

20

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 397 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
25   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

30

```
CTGAACTCTA CCTGGTGACC AGGGACCAGG ACCTTTATAA GGTGGAAGGC TTGATGTCCT    60
CCCCAGACTC AGCTCCTGGT GAAGCTCCCA GCCATCAGCC ATGAGGGTCT TGTATCTCCT   120
CTTCTCGTTC CTCTTCATAT TCCTGATGCC TCTTCCAGGT GTTTTTGGTG GTATAGGCGA   180
TCCCGTTACC TGCCTTAAGA GTGGAGCCAT ATGTCATCCA GTCTTTTGCC CTAGAAGGTA   240
TAAACNAATT GGCACCTGTG GTCTCCCTGG AACAAAATGC TGNAAAAAGC CATGAGGAGG   300
CCAAGAAGCT GCTGTGGCNG ANGCGGATTC AGAAAGGGCT CCCTCATCAG AGANGTGCGA   360
CATGTAAACC AAATTAAACT ATGGTGTCCA ANGATAN                            397
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